

SEQUENCE LISTING

<110> REGENTS OF THE UNIVERSITY OF CALIFORNIA
 TSIEN, Roger
 Campbell, Robert

<120> NON-OLIGOMERIZING FLUORESCENT PROTEINS

<130> REGEN1530-2

<140> Herewith

<141> 2001-05-24

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 716

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

<222> (1)..(714)

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gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cag	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	

gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	

130	135	140	
tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga			480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
145	150	155	160
atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt			528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
165	170		175
caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct			576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro			
180	185		190
gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg			624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			
195	200		205
aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta			672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val			
210	215		220
aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa ta			716
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys			
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 <213> Aequorea victoria

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20	25		30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35	40		45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe			
50	55		60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90		95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100	105		110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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 <222> (1)..(720)

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

65	70	75	80	
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac				480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc				528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	165	170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc				576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180	185	190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg				624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	195	200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc				672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210	215	220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa				720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	225	230	235	

<210> 4

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<212> PRT

<213> Aequorea victoria

<400> 4

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
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20	25	30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

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gtc gag ctg gac ggc gac gta aac ggc cac agg ttc agc gtg tcc ggc				96
Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly				
20		25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc				144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35		40	45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc				192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				
50		55	60	
ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag				240
Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys				
65		70	75	80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
85		90	95	
cgt acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
100		105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
115		120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
130		135	140	
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac				480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn				
145		150	155	160
ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc agc				528
Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser				
165		170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc				576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly				
180		185	190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg				624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu				
195		200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc				672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe				
210		215	220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa				720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys				
225		230	235	

<210> 6

<211> 239

<212> PRT

<213> Aequorea victoria

<400> 6

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tac ggc gtg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720
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<213> Aequorea victoria
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20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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<220>
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 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 10

<211> 239

<212> PRT

<213> Aequorea victoria

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 11
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<212> DNA
<213> Discosoma sp.

<220>
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<222> (54)..(731)

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Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
5 10 15

atg gaa gga acg gtc aat ggg cac gag ttt gaa ata gaa ggc gaa gga 152
Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggg agg cca tac gaa ggc cac aat acc gta aag ctt aag gta acc 200
Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val Thr
35 40 45

aag ggg gga cct ttg cca ttt gct tgg gat att ttg tca cca caa ttt 248
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60 65
cag tat gga agc aag gta tat gtc aag cac cct gcc gac ata cca gac 296
Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro Asp
70 75 80
tat aaa aag ctg tca ttt cct gaa gga ttt aaa tgg gaa agg gtc atg 344
Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95
aac ttt gaa gac ggt ggc gtc gtt act gta acc cag gat tcc agt ttg 392
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110
cag gat ggc tgt ttc atc tac aag gtc aag ttc att ggc gtg aac ttt 440
Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn Phe
115 120 125
cct tcc gat gga cct gtt atg caa aag aag aca atg ggc tgg gaa gcc 488
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
130 135 140 145
agc act gag cgt ttg tat cct cgt gat ggc gtg ttg aaa gga gag att 536
Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu Ile
150 155 160
cat aag gct ctg aag ctg aaa gac ggt ggt cat tac cta gtt gaa ttc 584
His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu Phe
165 170 175
aaa agt att tac atg gca aag aag cct gtg cag cta cca ggg tac tac 632
Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr Tyr
180 185 190
tat gtt gac tcc aaa ctg gat ata aca agc cac aac gaa gac tat aca 680
Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr
195 200 205
atc gtt gag cag tat gaa aga acc gag gga cgc cac cat ctg ttc ctt 728
Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu
210 215 220 225
taa ggctgaactt ggctcagacg tgggtgagcg gtaatgacca caaaaggcag 781
cgaagaaaaa ccatgatcgt tttttttagg ttggcagcct gaaatcgtag gaaatacatc 841
agaaatgtta caaacagg 859

<210> 12
<211> 225
<212> PRT
<213> Discosoma sp.

<400> 12

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
1 5 10 15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
20 25 30

Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
35 40 45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
50 55 60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
65 70 75 80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
85 90 95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
100 105 110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
130 135 140

Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
145 150 155 160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
165 170 175

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
180 185 190

Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
195 200 205

Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
210 215 220

Leu
225

<210> 13
<211> 42
<212> DNA

<213> Artificial

<220>

<223> PRIMER A206K top

<400> 13

cagtccaagc tgagcaaaga ccccaacgag aagcgcgatc ac

42

<210> 14

<211> 42

<212> DNA

<213> Artificial

<220>

<223> PRIMER A206K bottom

<400> 14

gtgatcgcgc ttctcgttgg ggtcttttgc cagcttggac tg

42

<210> 15

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PRIMER L221K top

<400> 15

cacatggtcc tgaaggagtt cgtgaccgcc gccggg

36

<210> 16

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PRIMER L221K bottom

<400> 16

cccggcggcg gtcacgaact ccttcaggac catgtg

36

<210> 17

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PRIMER F223R top

<400> 17

cacatggtcc tgctggagcg cgtgaccgcc gccggg

36

<210> 18

<211> 36

<212> DNA

<213> Artificial

<220>
 <223> PRIMER F223R bottom

<400> 18
 cccggcggcg gtcacgcgct ccagcaggac catgtg 36

<210> 19
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER L221K/F223R top

<400> 19
 cacatcgtcc tgaaggagcg cgtgaccgcc gccggg 36

<210> 20
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER L221K/F223R bottom

<400> 20
 cccggcggcg gtcacgcgct ccttcaggac catgtg 36

<210> 21
 <211> 33
 <212> PRT
 <213> Artificial

<220>
 <223> ADDITIONAL 33 AMINO ACIDS TAG TO THE N-TERMINUS OF THE GFPs

<400> 21

Met Arg Gly Ser His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

Pro

<210> 22
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER I125K

<400> 22
 tacaaggtga agttcaaggc cgtgaacttc ccc 33

<210> 23
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER L125K reverse

<400> 23
 ggggaagttc acgcccttga acttcacctt gta 33

<210> 24
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER I125R forward

<400> 24
 tacaaggtga agttccgcgg cgtgaacttc ccc 33

<210> 25
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER I125R reverse

<400> 25
 ggggaagttc acgccgcgga acttcacctt gta 33

<210> 26
 <211> 18
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic peptide

<400> 26

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 1 5 10 15

Lys Gly

<210> 27
 <211> 86
 <212> DNA
 <213> Artificial

<220>
 <223> Primer for PCR

<400> 27
ccggatcccc ttggtgctg cctctccgc tgccaggctt gccgtgccg ctggtgctgc 60
caaggaacag atggtggcgt cctcgc 86

<210> 28
<211> 86
<212> DNA
<213> Artificial

<220>
<223> Primer for PCR

<400> 28
ccggatcccc ctggtgctg cctccccgc tgccgggctt cccgtcccg ctggtgctgc 60
ccaggaacag gtggtggcgg cctcgc 86

<210> 29
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer for PCR

<400> 29
gtacgacgat gacgataagg atcc 24